

39. A method for transforming a cell comprising transforming a cell with the polynucleotide of claim 31.
40. A cell comprising the chimeric gene of claim 37.
41. A method for producing a plant comprising transforming a plant cell with the chimeric gene of claim 31 and regenerating a plant from the transformed plant cell.
42. A plant comprising the chimeric gene of claim 37.
43. A seed comprising the chimeric gene of claim 37.
44. An isolated polynucleotide comprising:
  - (a) a nucleotide sequence encoding an lysyl-tRNA synthetase, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:16 have at least 90% identity based on the Clustal alignment method, or
  - (b) the complement of the nucleotide sequence.
45. The polynucleotide of claim 44, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:16 have 95% identity based on the Clustal alignment method.
46. The polynucleotide of claim 44 comprising the nucleotide sequence of SEQ ID NO:15.
47. The polynucleotide of claim 44, wherein the synthetase comprises the amino acid sequence of SEQ ID NO:16.
48. A chimeric gene comprising the polynucleotide of claim 44 operably linked to a regulatory sequence.
49. A vector comprising the polynucleotide of claim 44.
50. A method for transforming a cell comprising transforming a cell with the polynucleotide of claim 44.
51. A cell comprising the chimeric gene of claim 48.
52. A method for producing a plant comprising transforming a plant cell with the chimeric gene of claim 44 and regenerating a plant from the transformed plant cell.
53. A plant comprising the chimeric gene of claim 48.
54. A seed comprising the chimeric gene of claim 48.
55. An isolated polynucleotide comprising:
  - (a) a nucleotide sequence encoding an lysyl-tRNA synthetase, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:12 have at least 85% identity based on the Clustal alignment method, or
  - (b) the complement of the nucleotide sequence.
56. The polynucleotide of claim 55, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:12 have 90% identity based on the Clustal alignment method.